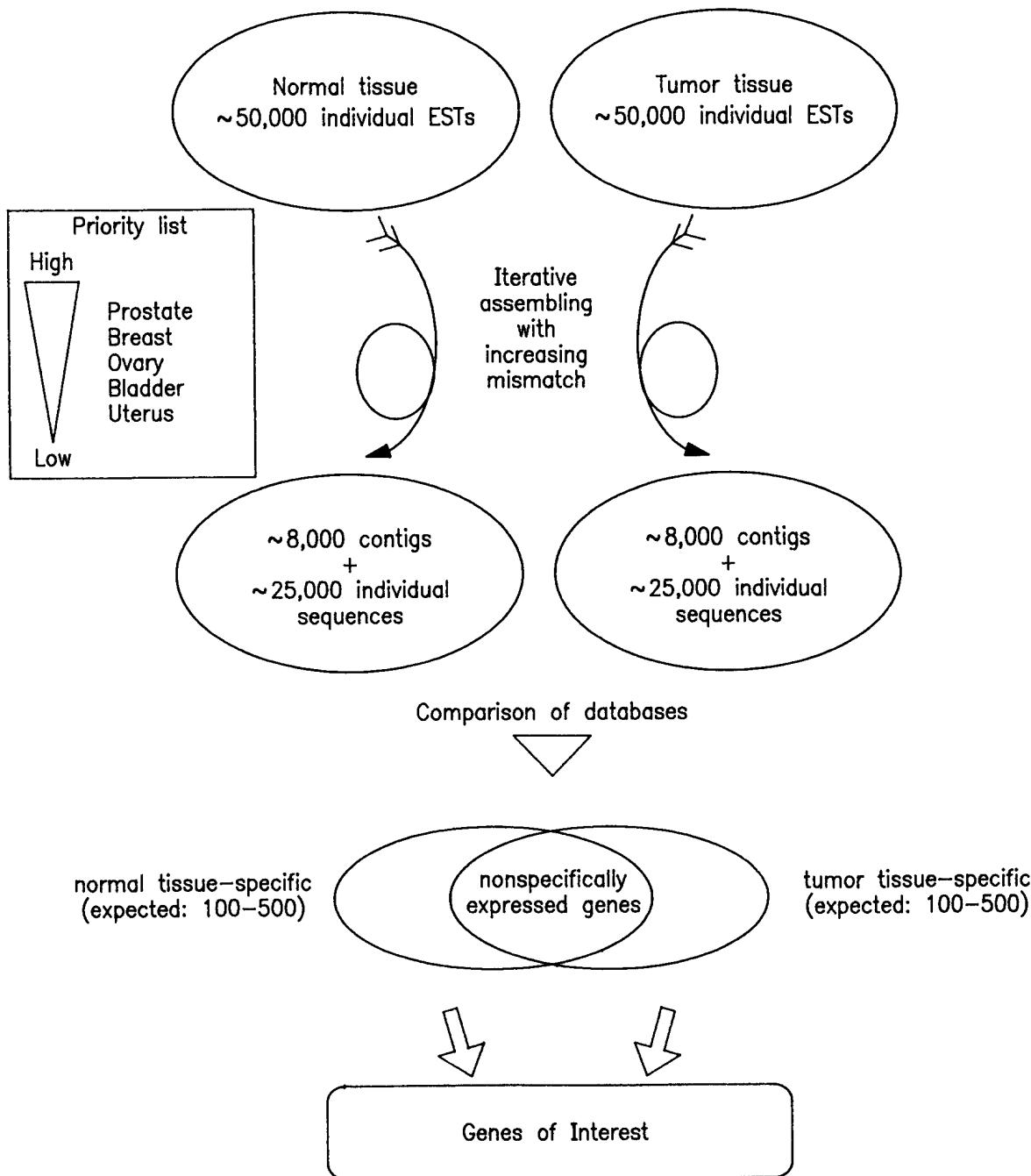


APPROVED	O. G. FIG.
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### Systematic Gene Search in the Incyte LifeSeq Database

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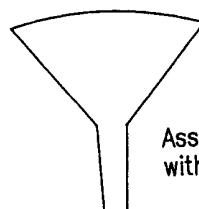


**FIG. I**

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## Principle of EST Assembly

 $\sim 50,000$  ESTs per tissueAssembly at 0% mismatch  
with GAP4 (Staden)

Contigs

Individual Sequences

Contigs increasing in  
number and lengthIterative assembly with  
increasing mismatch  
(1%, 2%, 4%)

5000–6000 Contigs

 $\sim 25,000$  other individual  
sequences $\sim 30,000$  consensus—  
sequences per tissue

FIG. 2a

09/673395-A-200

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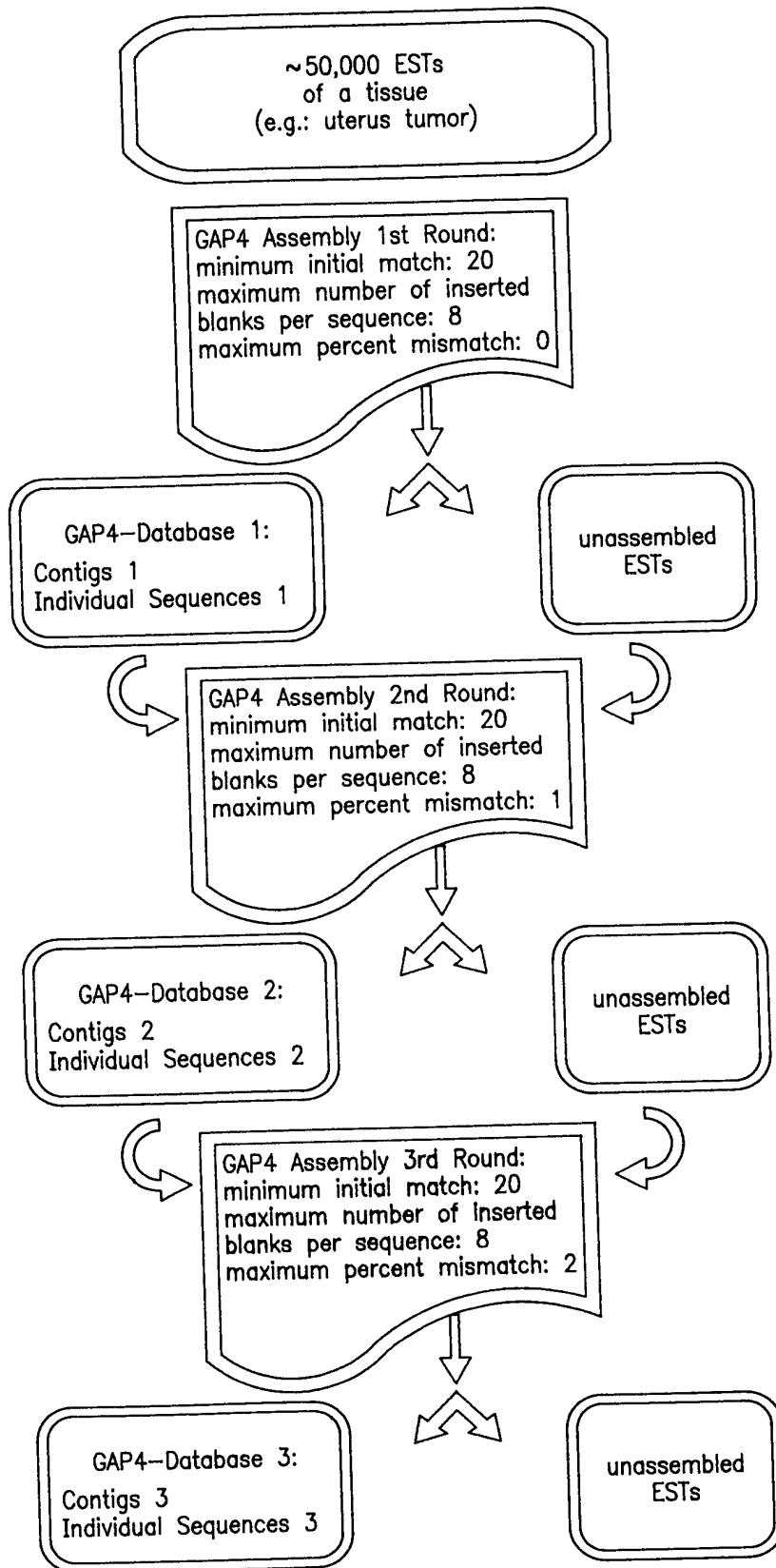


FIG. 2b-I

APPROVED BY	O. G. FIG.
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DRAFTSMAN	SUBCLASS

2002234567890

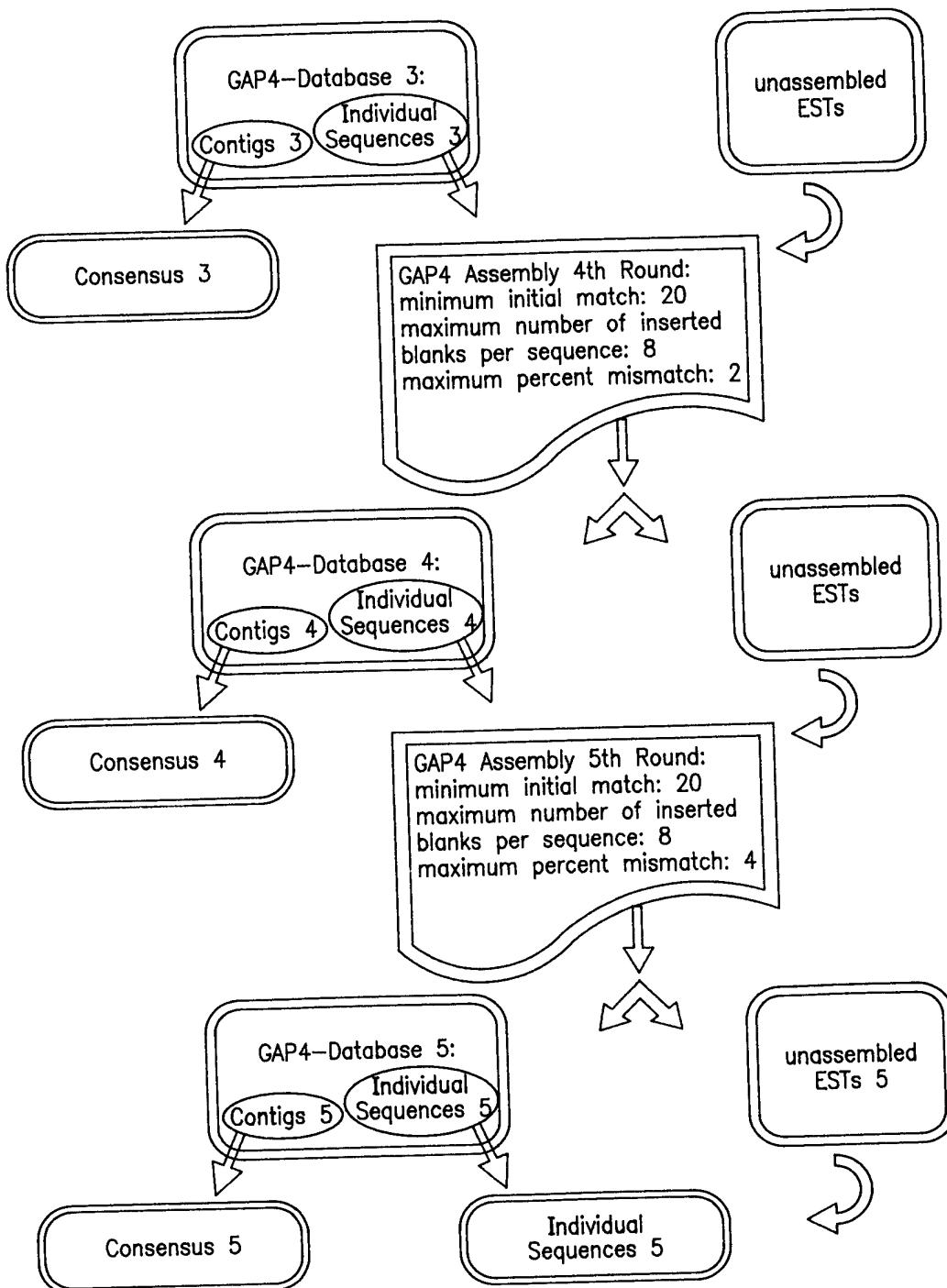


FIG. 2b-2

APPROVED	O. G. FIG.
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0962386 4222700

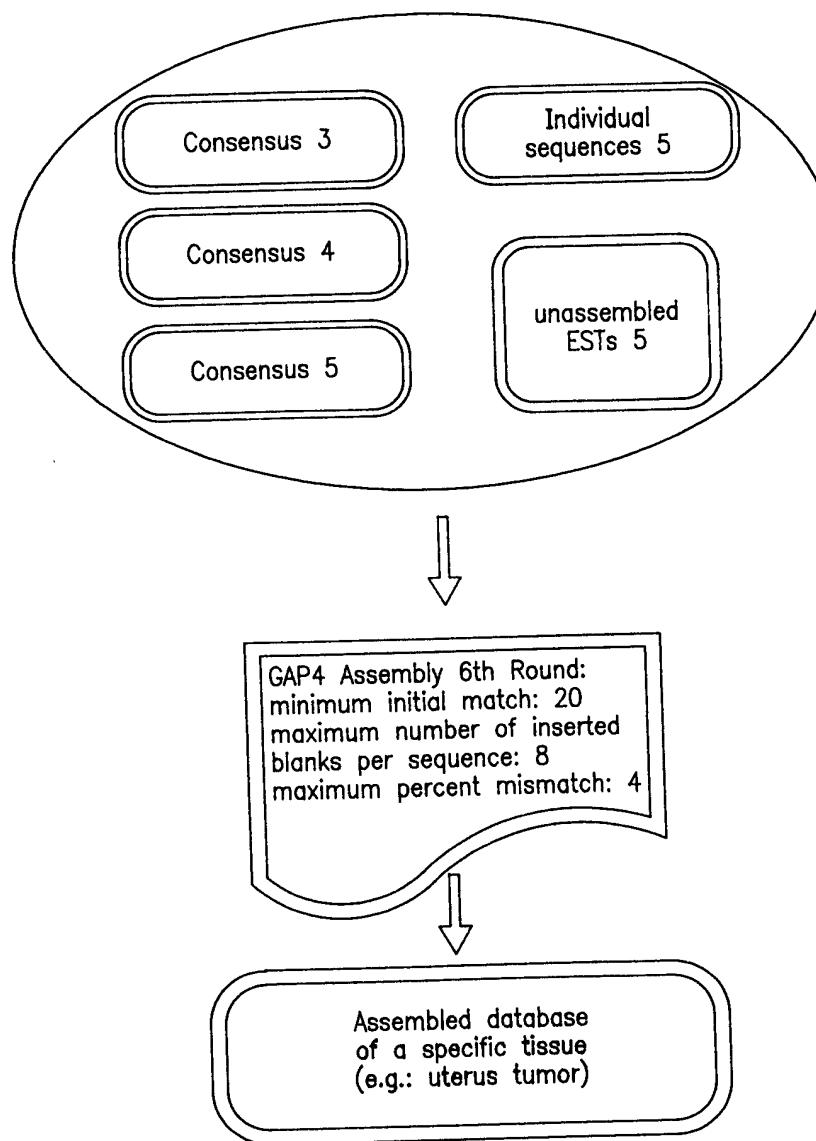


FIG. 2b-3

APPROVED	O. G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

662368-432700

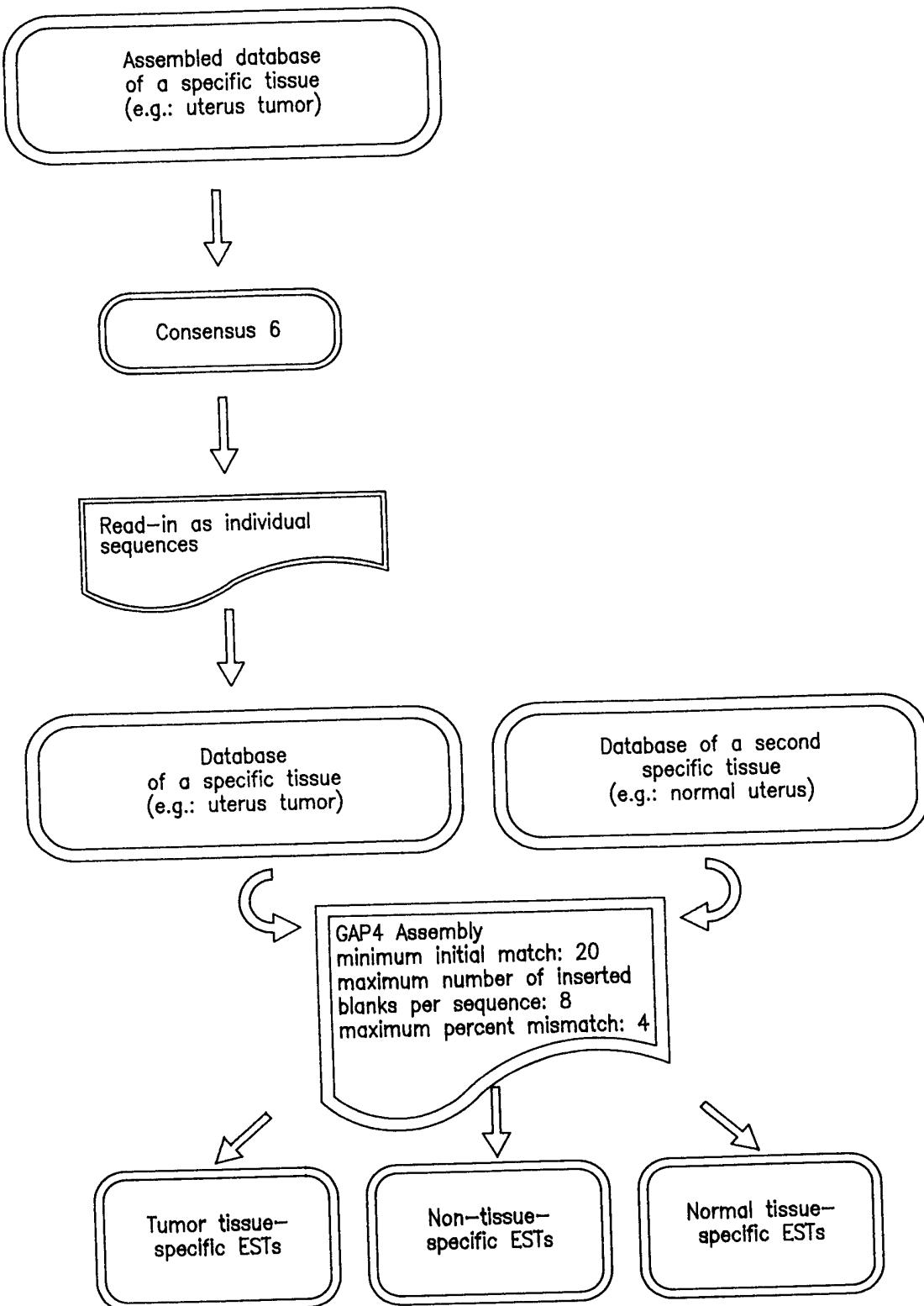


FIG. 2b-4

APPROVED BY DRAFTSMAN	O. G. FIG. CLASS	SUBCLASS
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## In silico subtraction of gene expression in various tissues

~30,000 consensus sequences  
normal tissue

~30,000 consensus sequences  
tumor tissue

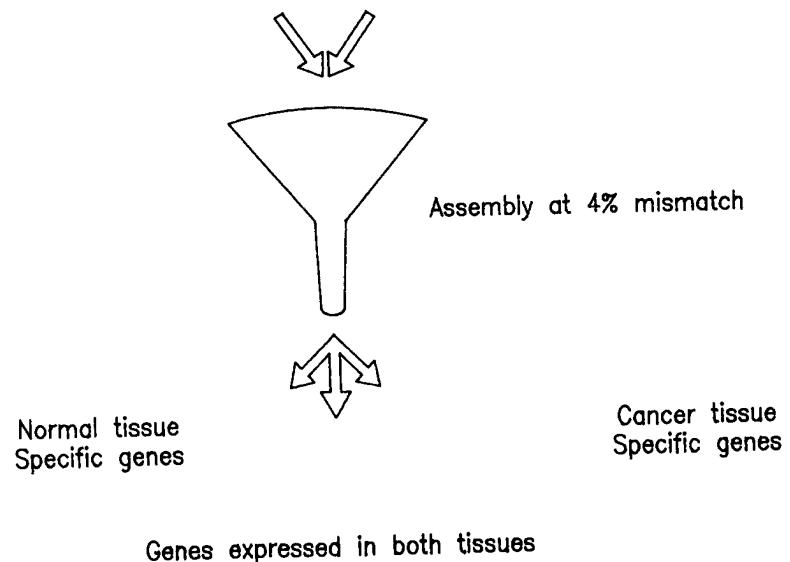


FIG. 3

APPROVED BY	O. G. FIG.
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600X2324 X 350 Y 100 Z 300 E 50

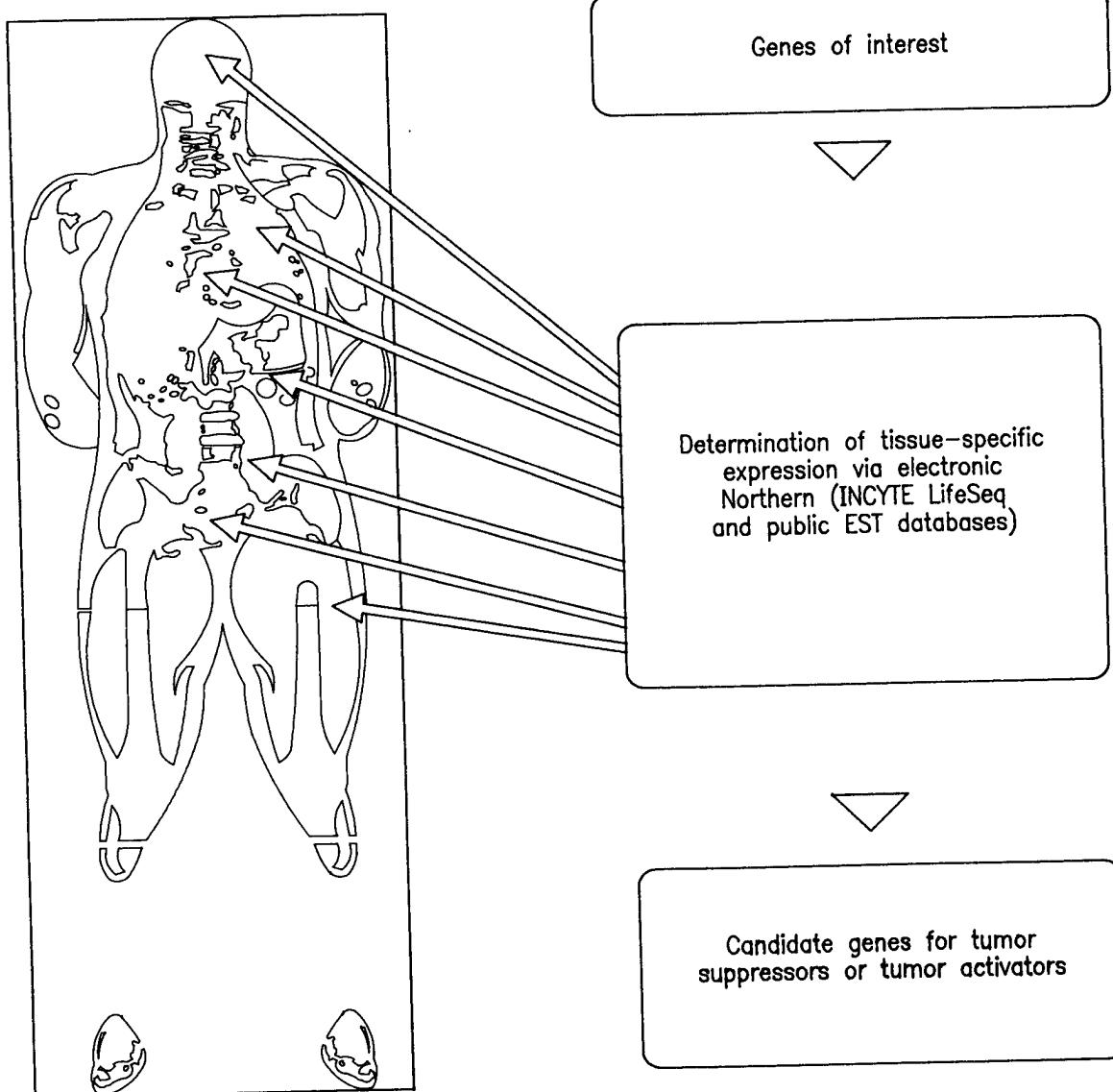


FIG. 4a

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

09/673395

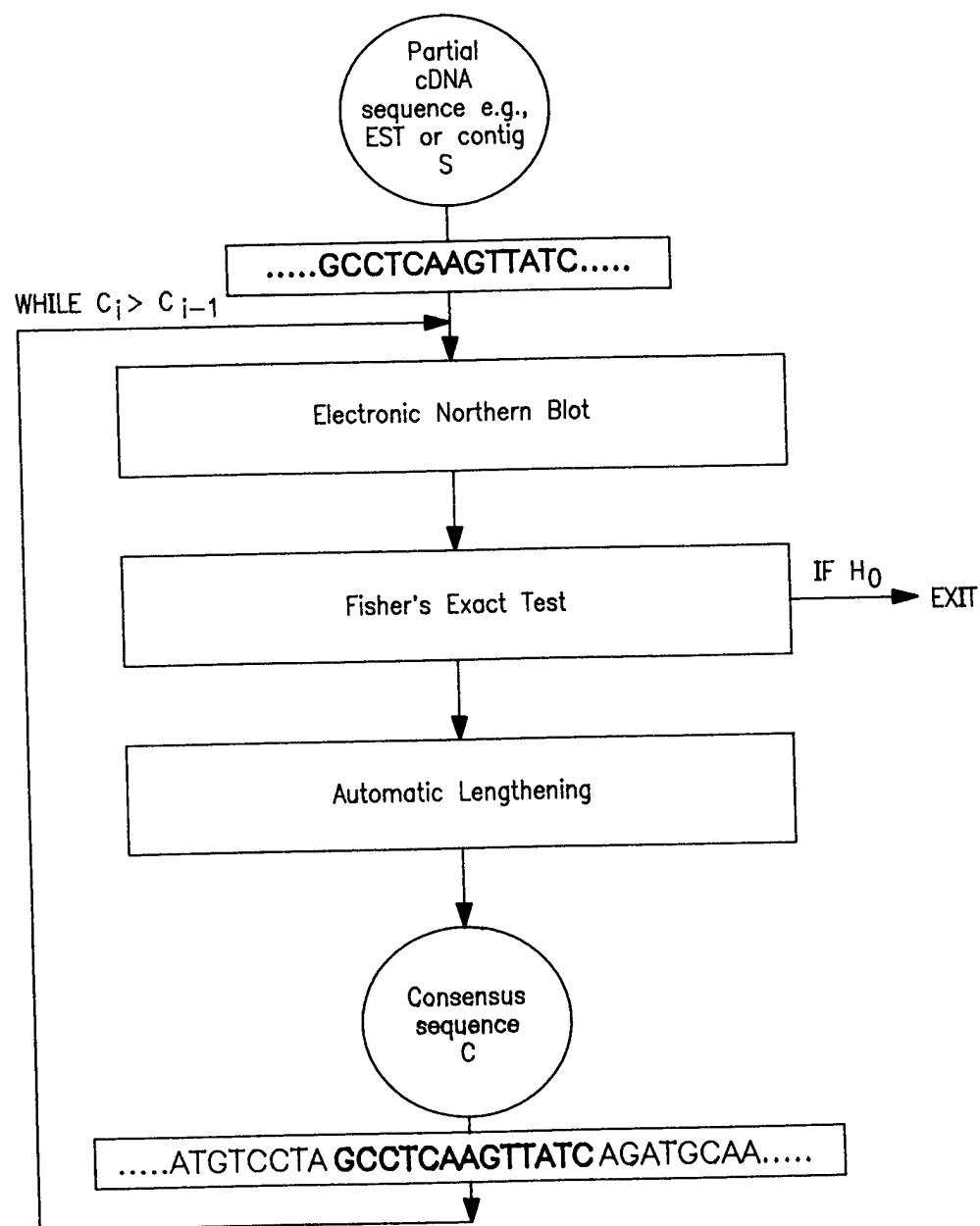


FIG. 4b

APPROVED	O G. FIG.
BY	CLASS SUBCLASS
M. A. MAN	

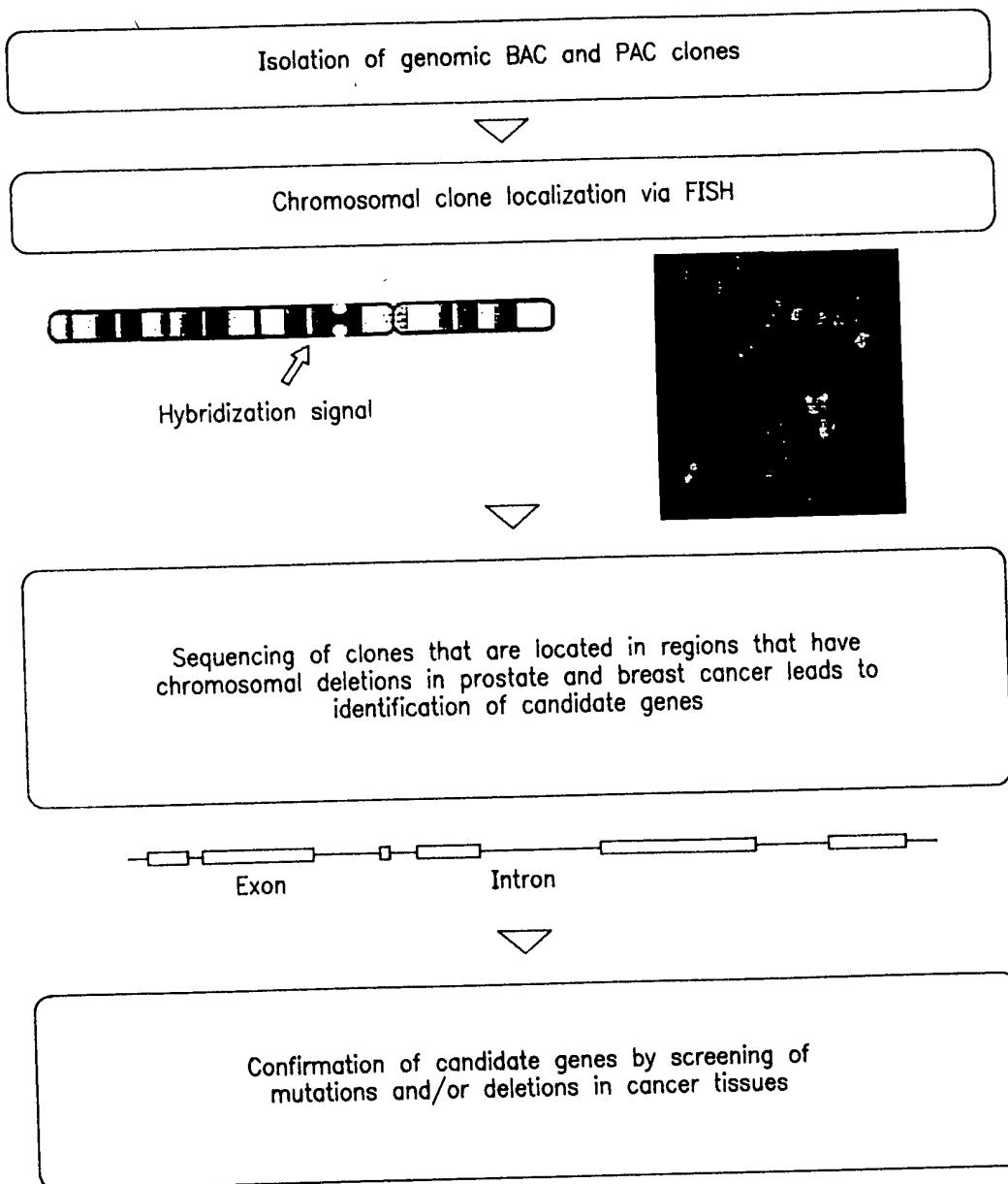


FIG. 5

002217-56662700